

GAP of: 0964DP54725 check: 3361 from: 1 to: 363

WPDEF Case 0964D Rad23 SwissProt P54725 Human Rad23A
Case 0964D Rad23 SwissProt P54725 Human Rad23A
P54725. UV excision repai. . .[gi:1709983] BLink, Domains, Links
LOCUS P54725 363 aa linear PRI 15-
SEP-2003
DEFINITION UV excision repair protein RAD23 homolog A (HHR23A).
ACCESSION P54725 . . .

to: 0964sid4 check: 9188 from: 1 to: 368

WPDEF Case 0964 Rad23 SEQ ID NO: 4 corn
Case 0964 Rad23 SEQ ID NO: 4 corn

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl.
Acad.
Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	537	Length:	393
Ratio:	1.479	Gaps:	8
Percent Similarity:	52.959	Percent Identity:	38.757

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

0964DP54725 x 0964sid4 October 28, 2003 11:27 ..

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      .
1 mavtitlktlqqqtfkirmepdetvkvkkekiaekgrdafpvaggqliy 50
  . :|.|||. |.||.:|.:|: .|. || .|:|.:.| | ||:
1 ..MKLTVKTLKGTHFEIRVQPNDTIMAVKKNIEEIQGKDSYPWGQQLLIF 48
      .
51 agkilsddvpirdyrideknfvvmvktkagqgtsappeasptaapess 100
  ||:| |: : : :.:| |.||||. | | | |
49 NGKVLKDESTLEENKVNEDGFLVVMLSKGKTSGSTGT.....SS 87
      .
101 tsfppaptsgmshpppaaredkspseesapttspesvsgsvpssgssgre 150
  . |. . | |.: | |. || . |..
88 SQHSNTPATRQAPPLEAPQQAPQPPVAPITTSQPEGLPAQAPNT.....H 132
      .
151 edaastlvtgseyetmlteismg...yerervvaalrasynnpgravey 197
  :.|||| |..| :|.: :.| || :.:.:| ||||.|||| |||||
133 DNAASNLLSGRNVDTIINQLMEMGGGSWDKDKVQRALRAAYNNPERAVEY 182
      .
198 lltgip.....gspepehgsvqesqvseqpate..... 225
  |.|||| |. : |. .| | |
183 LYSGIPVTAEIAVPIGGQGANTTDRAPTGEAGLSGIPNTAPLDLFPQGAS 232
      .
      .
      .
      .

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226aagenpleflrdqppqfqnmrqviqqnpallpallqqlgqenpqllq 271
 || ||:||||. |||| .|:..: || :| :| :| ..:||||:|.

233 NAGGGAGGGPLDFLRNNPQFQAVREMVHTNPQILQPMLVELSKQNPQILR 282

272 qisrhqe qfiqmlnep.pg eladis dveg evgaig eeapq mnyi qvtpqe 320
 | . :|:|:| || | | | | :| | . | |||:|

283 LIEENHDEFLQLLNEPFEGGEGDFLDQPEE.....DEMP..HAISVTPEE 325

321 keaierlkalgfpeslviqayfaceknenlaanflsqnfdde 363
 .||| ||..:|| . ||:|: ||:| ||||:|| :|:

326 QEAIGRLESMGFDRARVIEAFLACDRNEELAANYLLEHAGEED 368